



SEQUENCE LISTING

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<110> VETIGEN  
LENZEN, Gerlinde  
STROSBURG, Arthur Donny  
SUGASAWA, Toshinari  
MOROOKA, Shigeaki

<120> MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS

<130> 53356-5001-US

<140> US 09/319,724  
<141> 1999-09-08

<150> EP 96402719.7  
<151> 1996-12-12

<150> PCT/EP97/07339  
<151> 1997-12-12

<160> 21

<170> PatentIn version 3.1

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<212> PRT  
<213> Homo sapiens

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35 40 45

Lys Val Lys Leu Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val  
50 55 60

Lys Trp Lys Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr  
65 70 75 80

Leu Asp Pro Ser Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe  
85 90 95

Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile

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115	120	125
Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys		
130	135	140
Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe		
145	150	155
Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile		
165	170	175
Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser		
180	185	190
Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn		
195	200	205
Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp		
210	215	220
Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys		
225	230	235
Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser		
245	250	255
Arg Ala Ile Pro Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe		
260	265	270
Phe Val Ile Leu Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn		
275	280	285
Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg		
290	295	300
Pro Ile Pro Glu Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys		
305	310	315
Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe		
325	330	335

Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe  
 340 345 350

Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr  
 355 360 365

Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln  
 370 375 380

Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met  
 385 390 395 400

Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe  
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Gly Ile Met Cys Gly Ala Ile  
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 gatgttaatc taactagtga aggaaagggtg aaactgggttc caaatactaa aatccagatg 180  
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 tatggatgga aacaggtgca tggagatgta tttagaccat caagtcaccc actgatattt 480  
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gatgaatatg gatggaaaca ggtgcatgga gatgtattta gaccatcaag tcacccactg	300
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caaggaggaa ggagatggat aaagcagatg tttattgggg cattccttat cccagctatg	540
gtgtgtggca ctgccttctt catcaatttc atagccattt attaccatgc ttcaagagcc	600
attccttttg gaacaatggg ggccgtttgt tgcacatgtt tttttgttat tcttcctcta	660
aatcttggtg gtacaatact tggccgaaat ctgtcaggtc agcccaactt tccttgctgt	720
gtcaatgctg tgccctgtcc tataccggag aaaaaatggg tcatggagcc tgcggttatt	780
gtttgcctgg gtggaatttt accttttggg tcaatcttta ttgaaatgta tttcatcttc	840

acgtctttct gggcatataa gatctattat gtctatggct tcatgatgct ggtgctgggt 900  
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gaaga 965

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atcttcttgg tgggcttagt ttcaatgatt ttaatgagaa cattaagaaa agattatgct 180  
cggtagagta aagaggaaga aatggatgat atggatagag acctaggaga tgaatatgga 240  
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Ser

<210> 6  
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His

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 Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp  
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 atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat aag tac 143  
 Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr  
 35 40 45  
  
 ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt cat tac 191  
 Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr  
 50 55 60  
  
 cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa ttt agt 239  
 His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser  
 65 70 75  
  
 ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act tac tgt 287

Gly 80	Leu	Asp	Ile	Lys	Phe 85	Lys	Asp	Asp	Val	Met 90	Pro	Ala	Thr	Tyr	Cys 95	
gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat gcc ata																335
Glu	Ile	Asp	Leu	Asp 100	Lys	Glu	Lys	Arg	Asp 105	Ala	Phe	Val	Tyr	Ala	Ile	
aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca ata tgg																383
Lys	Asn	His	Tyr 115	Trp	Tyr	Gln	Met	Tyr 120	Ile	Asp	Asp	Leu	Pro	Ile	Trp	
ggt att gtt ggt gag gct gat gaa aat gga gaa gat tac tat ctt tgg																431
Gly	Ile	Val 130	Gly	Glu	Ala	Asp	Glu	Asn 135	Gly	Glu	Asp	Tyr	Tyr	Leu	Trp	
acc tat aaa aaa ctt gaa ata ggt ttt aat gga aat cga att gtt gat																479
Thr	Tyr	Lys	Lys	Leu	Glu	Ile	Gly	Phe 150	Asn	Gly	Asn	Arg	Ile	Val	Asp	
gtt aat cta act agt gaa gga aag gtg aaa ctg gtt cca aat act aaa																527
Val	Asn	Leu	Thr	Ser	Glu	Gly	Lys	Val 165	Lys	Leu	Val	Pro	Asn	Thr	Lys 175	
atc cag atg tca tat tca gta aaa tgg aaa aag tca gat gtg aaa ttt																575
Ile	Gln	Met	Ser 180	Tyr	Ser	Val	Lys	Trp 185	Lys	Lys	Ser	Asp	Val	Lys	Phe 190	
gaa gat cga ttt gac aaa tat ctt gat ccg tcc ttt ttt caa cat cgg																623
Glu	Asp	Arg	Phe 195	Asp	Lys	Tyr	Leu	Asp 200	Pro	Ser	Phe	Phe	Gln	His	Arg	
att cat tgg ttt tca att ttc aac tcc ttc atg atg gtg atc ttc ttg																671
Ile	His	Trp 210	Phe	Ser	Ile	Phe	Asn	Ser 215	Phe	Met	Met	Val	Ile	Phe	Leu	
gtg ggc tta gtt tca atg att tta atg aga aca tta aga aaa gat tat																719
Val	Gly	Leu	Val	Ser	Met	Ile	Leu	Met 230	Arg	Thr	Leu	Arg	Lys	Asp	Tyr 235	
gct cgg tac agt aaa gag gaa gaa atg gat gat atg gat aga gac cta																767
Ala	Arg	Tyr	Ser	Lys	Glu	Glu	Glu	Met 245	Asp	Asp	Met	Asp	Arg	Asp	Leu 255	
gga gat gaa tat gga tgg aaa cag gtg cat gga gat gta ttt aga cca																815
Gly	Asp	Glu	Tyr 260	Gly	Trp	Lys	Gln	Val 265	His	Gly	Asp	Val	Phe	Arg	Pro 270	
tca agt cac cca ctg ata ttt tcc tct ctg att ggt tct gga tgt cag																863
Ser	Ser	His	Pro 275	Leu	Ile	Phe	Ser	Ser 280	Leu	Ile	Gly	Ser	Gly	Cys	Gln 285	
ata ttt gct gtg tct ctc atc gtt att att gtt gca atg ata gaa gat																911
Ile	Phe	Ala	Val 290	Ser	Leu	Ile	Val	Ile 295	Ile	Val	Ala	Met	Ile	Glu	Asp 300	
tta tat act gag agg gga tca atg ctc agt aca gcc ata ttt gtc tat																959
Leu	Tyr	Thr	Glu	Arg	Gly	Ser	Met	Leu	Ser	Thr	Ala	Ile	Phe	Val	Tyr	



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gct gct acg tct cca gtg aat ggt tat ttt gga gga agt ctg tat gct Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala 320 325 330 335			1007
aga caa gga gga agg aga tgg ata aag cag atg ttt att ggg gca ttc Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe 340 345 350			1055
ctt atc cca gct atg gtg tgt ggc act gcc ttc ttc atc aat ttc ata Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile 355 360 365			1103
gcc att tat tac cat gct tca aga gcc att cct ttt gga aca atg gtg Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val 370 375 380			1151
gcc gtt tgt tgc atc tgt ttt ttt gtt att ctt cct cta aat ctt gtt Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val 385 390 395			1199
ggt aca ata ctt ggc cga aat ctg tca ggt cag ccc aac ttt cct tgt Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys 400 405 410 415			1247
cgt gtc aat gct gtg cct cgt cct ata ccg gag aaa aaa tgg ttc atg Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met 420 425 430			1295
gag cct gcg gtt att gtt tgc ctg ggt gga att tta cct ttt ggt tca Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser 435 440 445			1343
atc ttt att gaa atg tat ttc atc ttc acg tct ttc tgg gca tat aag Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys 450 455 460			1391
atc tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc ctg tgc Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys 465 470 475			1439
att gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta cta aat Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn 480 485 490 495			1487
gca gaa gat tac cgg tgg caa tgg aca agt ttt ctc tct gct gca tca Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser 500 505 510			1535
act gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt ttc aaa Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys 515 520 525			1583
aca aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga tat atg Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met 530 535 540			1631

gcg gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att ggt tac 1679  
 Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr  
 545 550 555

atg gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg aaa att 1727  
 Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile  
 560 565 570 575

gac tagagaccca agaaaacctg gaactttgga tcaatttctt tttcataggg 1780  
 Asp

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 <212> PRT  
 <213> Homo sapiens

<400> 14

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Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe  
 35 40 45

Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His  
 50 55 60

Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly  
 65 70 75 80

Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu  
 85 90 95

Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys  
 100 105 110

Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly  
 115 120 125

Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr  
 130 135 140

Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val  
 145 150 155 160

Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr Lys Ile  
 165 170 175

Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys Phe Glu  
 180 185 190

Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His Arg Ile  
 195 200 205

His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Val  
 210 215 220

Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala  
 225 230 235 240

Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly  
 245 250 255

Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg Pro Ser  
 260 265 270

Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile  
 275 280 285

Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu  
 290 295 300

Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala  
 305 310 315 320

Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg  
 325 330 335

Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu  
 340 345 350

Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe Ile Ala  
 355 360 365

Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met Val Ala  
 370 375 380

Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu Val Gly  
 385 390 395 400

Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro Cys Arg  
 405 410 415

Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe Met Glu  
 420 425 430

Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile  
 435 440 445

Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile  
 450 455 460

Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile  
 465 470 475 480

Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala  
 485 490 495

Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr  
 500 505 510

Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr  
 515 520 525

Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala  
 530 535 540

Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly Tyr Met  
 545 550 555 560

Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp  
 565 570 575

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<220>

<221> MISC\_FEATURE

<223> SM binding protein

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Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys  
35 40 45

Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser His  
50 55 60

Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu Phe  
65 70 75 80

Ser Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr Tyr  
85 90 95

Cys Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala  
100 105 110

Ile Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile  
115 120 125

Trp Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu  
130 135 140

Trp Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile Val  
145 150 155 160

Asp Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn Thr  
165 170 175

Lys Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val Lys  
180 185 190

Phe Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln His

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Arg Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile Phe 210 215 220		
Leu Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys Asp 225 230 235 240		
Tyr Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg Asp 245 250 255		
Leu Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe Arg 260 265 270		
Pro Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly Cys 275 280 285		
Gln Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile Glu 290 295 300		
Asp Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe Val 305 310 315 320		
Tyr Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu Tyr 325 330 335		
Ala Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly Ala 340 345 350		
Phe Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn Phe 355 360 365		
Ile Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr Met 370 375 380		
Val Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn Leu 385 390 395 400		
Val Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe Pro 405 410 415		
Cys Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp Phe 420 425 430		

Met Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe Gly  
435 440 445

Ser Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala Tyr  
450 455 460

Lys Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile Leu  
465 470 475 480

Cys Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu  
485 490 495

Asn Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala  
500 505 510

Ser Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe  
515 520 525

Lys Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr  
530 535 540

Met Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile Gly  
545 550 555 560

Tyr Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val Lys  
565 570 575

Ile Asp

<210> 16  
<211> 589  
<212> PRT  
<213> Arabidopsis thaliana

<220>  
<221> misc\_feature  
<223> endomembrane protein 70

<400> 16

Met Pro Ser Ser Ser Ser Ala Ala Val Leu Val Phe Leu Leu Leu Val  
1 5 10 15

Ser Leu Leu Thr Pro Thr Phe Ala Ser Asp Ser Asp His Lys Tyr Gln  
 20 25 30

Ala Glu Glu Gln Val Thr Leu Trp Val Asn Lys Val Gly Pro Tyr Asn  
 35 40 45

Asn Pro Gln Glu Thr Tyr Asn Tyr Tyr Ser Leu Pro Phe Cys Arg Pro  
 50 55 60

Ser Gly Asn Asn Val His Lys Trp Gly Gly Leu Gly Glu Val Leu Gly  
 65 70 75 80

Gly Asn Glu Leu Ile Asp Ser Glu Ile Ala Ile Lys Phe Met Lys Asn  
 85 90 95

Val Glu Arg Ser Val Ile Cys Pro Leu Glu Leu Asp Glu Ala Lys Val  
 100 105 110

Lys His Phe Lys Asp Ala Ile Glu Ser Ser Tyr Trp Phe Glu Phe Phe  
 115 120 125

Met Gly Met Phe His Val Cys Cys Phe Val Gly Glu Leu His Pro Asp  
 130 135 140

Lys Asn Ser Glu Asn Gly Lys His Val Leu Tyr Thr His Lys Asn Ile  
 145 150 155 160

Val Val Lys Tyr Asn Lys Asp Gln Ile Ile His Val Asn Leu Thr Gln  
 165 170 175

Asp Asn Pro Arg Pro Leu Glu Ala Gly Lys Lys Met Asp Leu Thr Tyr  
 180 185 190

Ser Val Gln Trp Ile Pro Thr Asn Val Thr Phe Ala Arg Arg Phe Asp  
 195 200 205

Val Tyr Leu Asp Tyr Pro Phe Phe Glu His Gln Ile His Trp Phe Ser  
 210 215 220

Ile Phe Asn Ser Phe Met Met Val Ile Phe Leu Thr Gly Leu Val Ser  
 225 230 235 240



Met Ile Leu Met Arg Thr Leu Arg Asn Asp Tyr Ala Lys Tyr Ala Arg  
 245 250 255

Glu Asp Asp Asp Leu Glu Ser Leu Glu Arg Asp Val Ser Glu Glu Ser  
 260 265 270

Gly Trp Lys Leu Val His Gly Asp Val Phe Arg Pro Ala Ser Ser Leu  
 275 280 285

Val Leu Leu Ser Ala Val Val Gly Thr Gly Ala Gln Leu Ala Leu Leu  
 290 295 300

Val Leu Leu Val Ile Leu Met Ala Ile Val Gly Thr Leu Tyr Val Gly  
 305 310 315 320

Arg Gly Ala Ile Val Thr Thr Phe Ile Val Cys Tyr Ala Leu Thr Ser  
 325 330 335

Phe Val Ser Gly Tyr Val Ser Gly Gly Met Tyr Ser Arg Ser Gly Gly  
 340 345 350

Lys His Trp Ile Lys Cys Met Val Leu Thr Ala Ser Leu Phe Pro Phe  
 355 360 365

Leu Cys Phe Gly Ile Gly Phe Leu Leu Asn Thr Ile Ala Ile Phe Tyr  
 370 375 380

Gly Ser Leu Ala Ala Ile Pro Phe Gly Thr Met Val Val Val Phe Val  
 385 390 395 400

Ile Trp Gly Phe Ile Ser Phe Pro Leu Ala Leu Leu Gly Thr Val Val  
 405 410 415

Gly Arg Asn Trp Ser Gly Ala Pro Asn Asn Pro Cys Arg Val Lys Thr  
 420 425 430

Ile Pro Arg Pro Ile Pro Glu Lys Lys Trp Tyr Leu Thr Pro Ser Val  
 435 440 445

Val Ser Leu Met Gly Gly Leu Leu Pro Phe Gly Ser Ile Phe Ile Glu  
 450 455 460

Met Tyr Phe Val Phe Thr Ser Phe Trp Asn Tyr Lys Val Tyr Tyr Val

465 470 475 480

Tyr Gly Phe Met Leu Leu Val Phe Val Ile Leu Val Ile Val Thr Val  
485 490 495

Cys Val Thr Ile Val Gly Thr Tyr Phe Leu Leu Asn Ala Glu Asn Tyr  
500 505 510

His Trp Gln Trp Thr Ser Phe Phe Ser Ala Ala Ser Thr Ala Val Tyr  
515 520 525

Val Tyr Leu Tyr Ser Ile Tyr Tyr Tyr Tyr Val Lys Thr Lys Met Ser  
530 535 540

Gly Phe Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Thr Met Met Phe Cys  
545 550 555 560

Leu Gly Leu Gly Ile Leu Cys Gly Ala Val Gly Tyr Leu Gly Ser Asn  
565 570 575

Leu Phe Val Arg Arg Ile Tyr Arg Asn Ile Lys Cys Asp  
580 585

<210> 17  
<211> 606  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> transmembrane 9 superfamily, protein member 1 precursor (hMP70)

<400> 17

Met Thr Val Val Gly Asn Pro Arg Ser Trp Ser Cys Gln Trp Leu Pro  
1 5 10 15

Ile Leu Ile Leu Leu Leu Gly Thr Gly His Gly Pro Gly Val Glu Gly  
20 25 30

Val Thr His Tyr Lys Ala Gly Asp Pro Val Ile Leu Tyr Val Asn Lys  
35 40 45

Val Gly Pro Tyr His Asn Pro Gln Glu Thr Tyr His Tyr Tyr Gln Leu  
50 55 60

Pro Val Cys Cys Pro Glu Lys Ile Arg His Lys Ser Leu Ser Leu Gly  
 65 70 75 80

Glu Val Leu Asp Gly Asp Arg Met Ala Glu Ser Leu Tyr Glu Ile Arg  
 85 90 95

Phe Arg Glu Asn Val Glu Lys Arg Ile Leu Cys His Met Gln Leu Ser  
 100 105 110

Ser Ala Gln Val Glu Gln Leu Arg Gln Ala Ile Glu Glu Leu Tyr Tyr  
 115 120 125

Phe Glu Phe Val Val Asp Asp Leu Pro Ile Arg Gly Phe Val Gly Tyr  
 130 135 140

Met Glu Glu Ser Gly Phe Leu Pro His Ser His Lys Ile Gly Leu Trp  
 145 150 155 160

Thr His Leu Asp Phe His Leu Glu Phe His Gly Asp Arg Ile Ile Phe  
 165 170 175

Ala Asn Val Ser Val Arg Asp Val Lys Pro His Ser Leu Asp Gly Leu  
 180 185 190

Arg Pro Asp Glu Phe Leu Gly Leu Thr His Thr Tyr Ser Val Arg Trp  
 195 200 205

Ser Glu Thr Ser Val Glu Arg Arg Ser Asp Arg Arg Arg Gly Asp Asp  
 210 215 220

Gly Gly Phe Phe Pro Arg Thr Leu Glu Ile His Trp Leu Ser Ile Ile  
 225 230 235 240

Asn Ser Met Val Leu Val Phe Leu Leu Val Gly Phe Val Ala Val Ile  
 245 250 255

Leu Met Arg Val Leu Arg Asn Asp Leu Ala Arg Tyr Asn Leu Asp Glu  
 260 265 270

Glu Thr Thr Ser Ala Gly Ser Gly Asp Asp Phe Asp Gln Gly Asp Asn  
 275 280 285

Gly Trp Lys Ile Ile His Thr Asp Val Phe Arg Phe Pro Pro Tyr Arg  
 290 295 300

Gly Leu Leu Cys Ala Val Leu Gly Val Gly Ala Gln Phe Leu Ala Leu  
 305 310 315 320

Gly Thr Gly Ile Ile Val Met Ala Leu Leu Gly Met Phe Asn Val His  
 325 330 335

Arg His Gly Ala Ile Asn Ser Ala Ala Ile Leu Leu Tyr Ala Leu Thr  
 340 345 350

Cys Cys Ile Ser Gly Tyr Val Ser Ser His Phe Tyr Arg Gln Ile Gly  
 355 360 365

Gly Glu Arg Trp Val Trp Asn Ile Ile Leu Thr Thr Ser Leu Phe Ser  
 370 375 380

Val Pro Phe Phe Leu Thr Trp Ser Val Val Asn Ser Val His Trp Ala  
 385 390 395 400

Asn Gly Ser Thr Cln Ala Leu Pro Ala Thr Thr Ile Leu Leu Leu Leu  
 405 410 415

Thr Val Trp Leu Leu Val Gly Phe Pro Leu Thr Val Ile Gly Gly Ile  
 420 425 430

Phe Gly Lys Asn Asn Ala Ser Pro Phe Asp Ala Pro Cys Arg Thr Lys  
 435 440 445

Asn Ile Ala Arg Glu Ile Asn Pro Gln Pro Trp Tyr Lys Ser Thr Asp  
 450 455 460

Ile His Met Thr Val Gly Gly Phe Leu Pro Phe Ser Ala Ile Ser Val  
 465 470 475 480

Glu Leu Tyr Tyr Ile Phe Ala Thr Val Trp Gly Arg Glu Gln Tyr Thr  
 485 490 495

Leu Tyr Gly Ile Leu Phe Phe Val Phe Ala Ile Leu Leu Ser Val Gly  
 500 505 510

Ala Ser Ile Ser Ile Ala Leu Thr Tyr Phe Gln Leu Ser Gly Glu Asp  
515 520 525

Tyr Arg Trp Trp Trp Arg Ser Val Leu Ser Val Gly Ser Thr Gly Leu  
530 535 540

Phe Ile Phe Leu Tyr Ser Val Phe Tyr Tyr Ala Arg Arg Ser Asn Met  
545 550 555 560

Ser Gly Ala Val Gln Thr Val Glu Phe Phe Gly Tyr Ser Leu Leu Thr  
565 570 575

Gly Tyr Val Phe Phe Leu Met Leu Gly Thr Ile Ser Phe Phe Ser Ser  
580 585 590

Leu Lys Phe Ile Arg Tyr Ile Tyr Val Asn Leu Lys Met Asp  
595 600 605

<210> 18  
<211> 662  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> multispanning membrane protein p76

<400> 18

Met Ser Ala Arg Leu Pro Val Leu Ser Pro Pro Arg Trp Pro Arg Leu  
1 5 10 15

Leu Leu Leu Ser Leu Leu Leu Leu Gly Ala Val Pro Gly Pro Arg Ser  
20 25 30

Gly Ala Phe Tyr Leu Pro Gly Leu Ala Pro Val Asn Phe Cys Asp Glu  
35 40 45

Glu Lys Lys Ser Asp Glu Cys Lys Ala Glu Ile Glu Leu Phe Val Asn  
50 55 60

Arg Leu Asp Ser Val Glu Ser Val Leu Pro Tyr Glu Tyr Thr Ala Phe  
65 70 75 80

Asp Phe Cys Gln Ala Ser Glu Gly Lys Arg Pro Ser Glu Asn Leu Gly

85	90	95
Gln Val Leu Phe Gly Glu Arg Ile Glu Pro Ser Pro Tyr Lys Phe Thr 100 105 110		
Phe Asn Lys Lys Glu Thr Cys Lys Leu Val Cys Thr Lys Thr Tyr His 115 120 125		
Thr Glu Lys Ala Glu Asp Lys Gln Lys Leu Glu Phe Leu Lys Lys Ser 130 135 140		
Met Leu Leu Asn Tyr Gln His His Trp Ile Val Asp Asn Met Pro Val 145 150 155 160		
Thr Trp Cys Tyr Asp Val Glu Asp Gly Gln Arg Phe Cys Asn Pro Gly 165 170 175		
Phe Pro Ile Gly Cys Tyr Ile Thr Asp Lys Gly His Ala Lys Asp Ala 180 185 190		
Cys Val Ile Ser Ser Asp Phe His Glu Arg Asp Thr Phe Tyr Ile Phe 195 200 205		
Asn His Val Asp Ile Lys Ile Tyr Tyr His Val Val Glu Thr Gly Ser 210 215 220		
Met Gly Ala Arg Leu Val Ala Ala Lys Leu Glu Pro Lys Ser Phe Lys 225 230 235 240		
His Thr His Ile Asp Lys Pro Asp Cys Ser Gly Pro Pro Met Asp Ile 245 250 255		
Ser Asn Lys Ala Ser Gly Glu Ile Lys Ile Ala Tyr Thr Tyr Ser Val 260 265 270		
Ser Phe Glu Glu Asp Asp Lys Ile Arg Trp Ala Ser Arg Trp Asp Tyr 275 280 285		
Ile Leu Glu Ser Met Pro His Thr His Ile Gln Trp Phe Ser Ile Met 290 295 300		
Asn Ser Leu Val Ile Val Leu Phe Leu Ser Gly Met Val Ala Met Ile 305 310 315 320		

Met Leu Arg Thr Leu His Lys Asp Ile Ala Arg Tyr Asn Gln Met Asp  
325 330 335

Ser Thr Glu Asp Ala Gln Glu Glu Phe Gly Trp Lys Leu Val His Gly  
340 345 350

Asp Ile Phe Arg Pro Pro Arg Lys Gly Met Leu Leu Ser Val Phe Leu  
355 360 365

Gly Ser Gly Thr Gln Ile Leu Ile Met Thr Phe Val Thr Leu Phe Phe  
370 375 380

Ala Cys Leu Gly Phe Leu Ser Pro Ala Asn Arg Gly Ala Leu Met Thr  
385 390 395 400

Cys Ala Val Val Leu Trp Val Leu Leu Gly Thr Pro Ala Gly Tyr Val  
405 410 415

Ala Ala Arg Phe Tyr Lys Ser Phe Gly Gly Glu Lys Trp Lys Thr Asn  
420 425 430

Val Leu Leu Thr Ser Phe Leu Cys Pro Gly Ile Val Phe Ala Asp Phe  
435 440 445

Phe Ile Met Asn Leu Ile Leu Trp Gly Glu Gly Ser Ser Ala Ala Ile  
450 455 460

Pro Phe Gly Thr Leu Val Ala Ile Leu Ala Leu Trp Phe Cys Ile Ser  
465 470 475 480

Val Pro Leu Thr Phe Ile Gly Ala Tyr Phe Gly Phe Lys Lys Asn Ala  
485 490 495

Ile Glu His Pro Val Arg Thr Asn Gln Ile Pro Arg Gln Ile Pro Glu  
500 505 510

Gln Ser Phe Tyr Thr Lys Pro Leu Pro Gly Ile Ile Met Gly Gly Ile  
515 520 525

Leu Pro Phe Gly Cys Ile Phe Ile Gln Leu Phe Phe Ile Leu Asn Ser  
530 535 540

Ile Trp Ser His Gln Met Tyr Tyr Met Phe Gly Phe Leu Phe Leu Val  
 545 550 555 560

Phe Ile Ile Leu Val Ile Thr Cys Ser Glu Ala Thr Ile Leu Leu Cys  
 565 570 575

Tyr Phe His Leu Cys Ala Glu Asp Tyr His Trp Gln Trp Arg Ser Phe  
 580 585 590

Leu Thr Ser Gly Phe Thr Ala Val Tyr Phe Leu Ile Tyr Ala Val His  
 595 600 605

Tyr Phe Phe Ser Lys Leu Gln Ile Thr Gly Thr Ala Ser Thr Ile Leu  
 610 615 620

Tyr Phe Gly Tyr Thr Met Ile Met Val Leu Ile Phe Phe Leu Phe Thr  
 625 630 635 640

Gly Thr Ile Gly Phe Phe Ala Cys Phe Trp Phe Val Thr Lys Ile Tyr  
 645 650 655

Ser Val Val Lys Val Asp  
 660

<210> 19  
 <211> 586  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> GenBank No. D87444

<400> 19

Met Arg Pro Leu Pro Gly Ala Leu Gly Val Ala Ala Ala Ala Leu Trp  
 1 5 10 15

Leu Leu Leu Leu Leu Leu Pro Arg Thr Arg Ala Asp Glu His Glu His  
 20 25 30

Thr Tyr Gln Asp Lys Glu Glu Val Val Leu Trp Met Asn Thr Val Gly  
 35 40 45



Pro Tyr His Asn Arg Gln Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe  
50 55 60

Cys Val Gly Ser Lys Lys Ser Ile Ser His Tyr His Glu Thr Leu Gly  
65 70 75 80

Glu Ala Leu Gln Gly Val Glu Leu Glu Phe Ser Gly Leu Asp Ile Lys  
85 90 95

Phe Lys Asp Asp Val Met Pro Ala Thr Tyr Cys Glu Ile Asp Leu Asp  
100 105 110

Lys Glu Lys Arg Asp Ala Phe Val Tyr Ala Ile Lys Asn His Tyr Trp  
115 120 125

Tyr Gln Met Tyr Ile Asp Asp Leu Pro Ile Trp Gly Ile Val Gly Glu  
130 135 140

Ala Asp Glu Asn Gly Glu Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu  
145 150 155 160

Glu Ile Gly Phe Asn Gly Asn Arg Ile Val Asp Val Asn Leu Thr Ser  
165 170 175

Glu Gly Lys Val Lys Leu Gly Ser Lys Tyr Tyr Asn Pro Asp Val Ile  
180 185 190

Phe Ser Lys Met Glu Lys Ser Asp Val Lys Phe Glu Asp Arg Phe Asp  
195 200 205

Asn Ile Leu Ile Val Leu Phe Ser His Arg Ile His Trp Phe Ser Ile  
210 215 220

Phe Asn Ser Phe Met Met Val Ile Phe Leu Val Gly Leu Val Ser Met  
225 230 235 240

Ile Leu Met Arg Thr Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu  
245 250 255

Glu Glu Met Asp Asp Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp  
260 265 270

Lys Gln Val His Gly Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile

275		280		285
Phe Ser Ser Leu Ile Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu	290	295	300	
Ile Val Ile Ile Val Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly	305	310	315	320
Ser Met Leu Ser Thr Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val	325	330	335	
Asn Gly Tyr Phe Gly Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg	340	345	350	
Trp Ile Lys Gln Met Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Gly	355	360	365	
Val His Cys Leu Leu His Gln Phe His Ser His Leu Leu Pro Cys Phe	370	375	380	
Lys Ser His Ser Phe Trp Asn Asn Gly Gly Arg Leu Leu His Leu Phe	385	390	395	400
Phe Cys Tyr Ser Ser Ser Lys Ser Cys Trp Tyr Asn Thr Trp Pro Lys	405	410	415	
Ser Val Arg Ser Ala Gln Leu Ser Leu Ser Cys Gln Cys Cys Ala Ser	420	425	430	
Ser Tyr Thr Gly Glu Lys Met Val His Gly Ala Ala Val Ile Val Cys	435	440	445	
Leu Gly Gly Ile Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe	450	455	460	
Ile Phe Thr Ser Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe	465	470	475	480
Met Met Leu Val Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr	485	490	495	
Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln	500	505	510	

Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met  
515 520 525

Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe  
530 535 540

Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu  
545 550 555 560

Gly Ile Met Cys Gly Ala Ile Gly Tyr Met Gly Thr Ser Ala Phe Val  
565 570 575

Arg Lys Ile Tyr Thr Asn Val Lys Ile Asp  
580 585

<210> 20  
<211> 667  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<220>  
<221> misc\_feature  
<223> Emp70 (p24a 70 kDa precursor)

<400> 20

Met Ile Tyr Lys Met Ala His Val Gln Leu Leu Leu Leu Tyr Phe Phe  
1 5 10 15

Val Ser Thr Val Lys Ala Phe Tyr Leu Pro Gly Val Ala Pro Thr Thr  
20 25 30

Tyr Arg Glu Asn Asp Asn Ile Pro Leu Leu Val Asn His Leu Thr Pro  
35 40 45

Ser Met Asn Tyr Gln His Lys Asp Glu Asp Gly Asn Asn Val Ser Gly  
50 55 60

Asp Lys Glu Asn Phe Leu Tyr Ser Tyr Asp Tyr Tyr Tyr Asn Arg Phe  
65 70 75 80

His Phe Cys Gln Pro Glu Lys Val Glu Lys Gln Pro Glu Ser Leu Gly  
85 90 95

Ser Val Ile Phe Gly Asp Arg Ile Tyr Asn Ser Pro Phe Gln Leu Asn  
 100 105 110

Met Leu Gln Glu Lys Glu Cys Glu Ser Leu Cys Lys Thr Val Ile Pro  
 115 120 125

Gly Asp Asp Ala Lys Phe Ile Asn Lys Leu Ile Lys Asn Gly Phe Phe  
 130 135 140

Gln Asn Trp Leu Ile Asp Gly Leu Pro Ala Ala Arg Glu Val Tyr Asp  
 145 150 155 160

Gly Arg Thr Lys Thr Ser Phe Tyr Gly Ala Gly Phe Asn Leu Gly Phe  
 165 170 175

Val Gln Val Thr Gln Gly Thr Asp Ile Glu Ala Thr Pro Lys Gly Ala  
 180 185 190

Glu Thr Thr Asp Lys Asp Val Glu Leu Glu Thr Arg Asn Asp Cys Asn  
 195 200 205

Met Val Lys Thr Tyr Glu Leu Pro Tyr Phe Ala Asn His Phe Asp Ile  
 210 215 220

Met Ile Glu Tyr His Asp Arg Gly Glu Gly Asn Tyr Arg Val Val Gly  
 225 230 235 240

Val Ile Val Glu Pro Val Ser Ile Lys Arg Ser Ser Pro Gly Thr Cys  
 245 250 255

Glu Thr Thr Gly Ser Pro Leu Met Leu Asp Glu Glu Asn Asp Asn Glu  
 260 265 270

Val Tyr Phe Thr Tyr Ser Val Lys Phe Asn Glu Ser Ala Thr Ser Trp  
 275 280 285

Ala Thr Arg Trp Asp Lys Tyr Leu His Val Tyr Asp Pro Ser Ile Gln  
 290 295 300

Trp Phe Ser Leu Ile Asn Phe Ser Leu Val Val Val Leu Leu Ser Ser  
 305 310 315 320

Val Val Ile His Ser Leu Leu Arg Ala Leu Lys Ser Asp Phe Ala Arg  
325 330 335

Tyr Asn Glu Leu Asn Leu Asp Asp Asp Phe Gln Glu Asp Ser Gly Trp  
340 345 350

Lys Leu Asn His Gly Asp Val Phe Arg Ser Pro Ser Gln Ser Leu Thr  
355 360 365

Leu Ser Ile Leu Val Gly Ser Gly Val Gln Leu Phe Leu Met Val Thr  
370 375 380

Cys Ser Ile Phe Phe Ala Ala Leu Gly Phe Leu Ser Pro Ser Ser Arg  
385 390 395 400

Gly Ser Leu Ala Thr Val Met Phe Ile Leu Tyr Ala Leu Phe Gly Phe  
405 410 415

Val Gly Ser Tyr Thr Ser Met Gly Ile Tyr Lys Phe Phe Asn Gly Pro  
420 425 430

Tyr Trp Lys Ala Asn Leu Ile Leu Thr Pro Leu Leu Val Pro Gly Ala  
435 440 445

Ile Leu Leu Ile Ile Ile Ala Leu Asn Phe Phe Leu Met Phe Val His  
450 455 460

Ser Ser Gly Val Ile Pro Ala Ser Thr Leu Phe Phe Met Val Phe Leu  
465 470 475 480

Trp Phe Leu Phe Ser Ile Pro Ser Ser Phe Ala Gly Ser Leu Ile Ala  
485 490 495

Arg Lys Arg Cys His Trp Asp Glu His Pro Thr Lys Thr Asn Gln Ile  
500 505 510

Ala Arg Gln Ile Pro Phe Gln Pro Trp Tyr Leu Lys Thr Ile Pro Ala  
515 520 525

Thr Leu Ile Ala Gly Ile Phe Pro Phe Gly Ser Ile Ala Val Glu Leu  
530 535 540

Tyr Phe Ile Tyr Thr Ser Leu Trp Phe Asn Lys Ile Phe Tyr Met Phe

545 550 555 560

Gly Phe Leu Phe Phe Ser Phe Leu Leu Leu Thr Leu Thr Ser Ser Leu  
565 570 575

Val Thr Ile Leu Ile Thr Tyr His Ser Leu Cys Leu Glu Asn Trp Lys  
580 585 590

Trp Gln Trp Arg Gly Phe Ile Ile Gly Gly Ala Gly Cys Ala Leu Tyr  
595 600 605

Val Phe Ile His Ser Ile Leu Phe Thr Lys Phe Lys Leu Gly Gly Phe  
610 615 620

Thr Thr Ile Val Leu Tyr Val Gly Tyr Ser Ser Val Ile Ser Leu Leu  
625 630 635 640

Cys Cys Leu Val Thr Gly Ser Ile Gly Phe Ile Ser Ser Met Leu Phe  
645 650 655

Val Arg Lys Ile Tyr Ser Ser Ile Lys Val Asp  
660 665

D8  
<210> 21  
<211> 15  
<212> PRT  
<213> artificial

<220>  
<223> N-terminus of ICYP receptor, for generating antibodies  
<400> 21

Phe Phe Gln His Arg Ile His Val Phe Ser Ile Phe Asn His Cys  
1 5 10 15

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